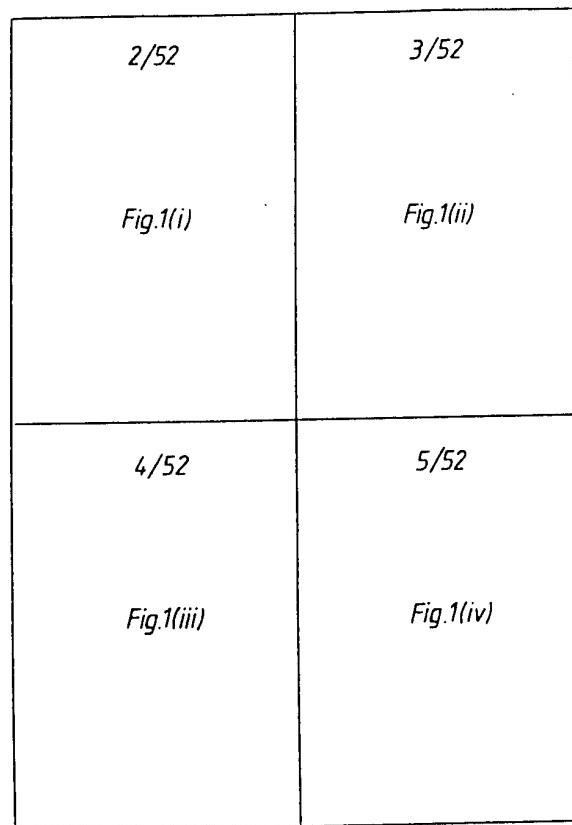


1/52



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1	TCGGCCTCC GAAACC ATG AAC TTT CTG Met Asn Phe Leu 1
50	CTT GCC TTG CTG CTC TAC CTC CAC Leu Ala Leu Leu Tyr Leu His 15
98	CCC ATG GCA GAA GGA GGA GGG CAG Pro Met Ala Glu Gly Gly Gln 30 35
146	ATG GAT GTC TAT CAG CGC AGC TAC Met Asp Val Tyr Gln Arg Ser Tyr 45 50
194	GAC ATC TTC CAG GAG TAC CCT GAT Asp Ile Phe Gln Glu Tyr Pro Asp 60 65
242	TCC TGT GTG CCC CTG ATG CGA TGC Ser Cys Val Pro Leu Met Arg Cys 80
290	CTC GAG TGT GTG CCC ACT GAG GAG Leu Glu Cys Val Pro Thr Glu Glu 95
338	CGG ATC AAA CCT CAC CAA GGC CAG Arg Ily Lys Pro His Gln Gly Gln 110 115

---

*Fig.1(i)*

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CTG TCT TGG GTG CAT TGG AGC	49
Leu Ser Trp Val His Trp Ser	
5	10
CAT GCC AAG TGG TCC CAG GCT GCA	97
His Ala Lys Trp Ser Gln Ala Ala	
20	25
AAT CAT CAC GAA GTG GTG AAG TTC	145
Asn His His Glu Val Val Lys Phe	
40	
TGC CAT CCA ATC GAG ACC CTG GTG	193
Cys His Pro Ile Glu Thr Leu Val	
55	
GAG ATC GAG TAC ATC TTC AAG CCA	241
Glu Ile Glu Tyr Ile Phe Lys Pro	
70	75
GGG GGC TGC TGC AAT GAC GAG GGC	289
Gly Gly Cys Cys Asn Asp Glu Gly	
85	90
TCC AAC ATC ACC ATG CAG ATT ATG	337
Ser Asn Ile Thr Met Gln Ile Met	
100	105
CAC ATA GGA GAG ATG AGC TTC CTA	385
His Ile Gly Glu Met Ser Phe Leu	
120	

Fig. 1(ii)

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386	CAG CAC AAC AAA TGT GAA TGC AGA Gln His Asn Lys Cys Glu Cys Arg 125	130
434	GAA AAT CCC TGT GGG CCT TGC TCA Glu Asn Pro Cys Gly Pro Cys Ser 140	145
482	CAA GAT CCG CAG ACG TGT AAA TGT Gln Asp Pro Gln Thr Cys Lys Cys 160	
530	TGC AAG GCG AGG CAG CTT GAG TTA Cys Lys Ala Arg Gln Leu Glu Leu 175	
578	AAG CCG AGG CGG TGAGCCGGGC AGGAG Lys Pro Arg Arg 190	
630	GAACCAGATC TCTCACCAAGG	

Fig.1(iii)

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CCA AAG AAA GAT AGA GCA AGA CAA Pro Lys Lys Asp Arg Ala Arg Gln 135	433
GAG CGG AGA AAG CAT TTG TTT GTA Glu Arg Arg Lys His Leu Phe Val 150	481
TCC TGC AAA AAC ACA GAC TCG CGT Ser Cys Lys Asn Thr Asp Ser Arg 165	529
AAC GAA CGT ACT TGC AGA TGT GAC Asn Glu Arg Thr Cys Arg Cys Asp 180	577
GAAGG AGCCTCCCTC AGCGTTTCGG	629
	649

Fig.1(iv)

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7/52	8/52
<i>Fig. 2(i)</i>	<i>Fig. 2(ii)</i>
9/52	10/52
<i>Fig. 2(iii)</i>	<i>Fig. 2(iv)</i>
11/52	12/52
<i>Fig. 2(v)</i>	<i>Fig. 2(vi)</i>

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1	CC ATG AGC CCT CTG CTC CGC CGC Met Ser Pro Leu Leu Arg Arg 1 5
48	CTG GCC CCC GCC CAG GCC CCT GTC Leu Ala Pro Ala Gln Ala Pro Val 20
96	CAG AGG AAA GTG GTG TCA TGG ATA Gln Arg Lys Val Val Ser Trp Ile 35
144	CAG CCC CGG GAG GTG GTG GTG CCC Gln Pro Arg Glu Val Val Val Pro 50 55
192	GTG GCC AAA CAG CTG GTG CCC AGC Val Ala Lys Gln Leu Val Pro Ser 65 70
240	GGC TGC TGC CCT GAC GAT GGC CTG Gly Cys Cys Pro Asp Asp Gly Leu 80 85
288	CAA GTC CGG ATG CAG ATC CTC ATG Gln Val Arg Met Gln Ile Leu Met 100
336	GGG GAG ATG TCC CTG GAA GAA CAC Gly Glu Met Ser Leu Glu Glu His 115

---

*Fig.2(i)*

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CTG CTG CTC GCC GCA CTC CTG CAG	47
Leu Leu Leu Ala Ala Leu Leu Gln	
10	15
TCC CAG CCT GAT GCC CCT GGC CAC	95
Ser Gln Pro Asp Ala Pro Gly His	
25	30
GAT GTG TAT ACT CGC GCT ACC TGC	143
Asp Val Tyr Thr Arg Ala Thr Cys	
40	45
TTG ACT GTG GAG CTC ATG GGC ACC	191
Leu Thr Val Glu Leu Met Gly Thr	
60	
TGC GTG ACT GTG CAG CGC TGT GGT	239
Cys Val Thr Val Gln Arg Cys Gly	
75	
GAG TGT GTG CCC ACT GGG CAG CAC	287
Glu Cys Val Pro Thr Gly Gln His	
90	95
ATC CGG TAC CCG AGC AGT CAG CTG	335
Ile Arg Tyr Pro Ser Ser Gln Leu	
105	110
AGC CAG TGT GAA TGC AGA CCT AAA	383
Ser Gln Cys Glu Cys Arg Pro Lys	
120	125

*Fig. 2(ii)*

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384	AAA AAG GAC AGT GCT GTG AAG CCA Lys Lys Asp Ser Ala Val Lys Pro 130	135
432	CGT CCC CAG CCC CGT TCT GTT CCG Arg Pro Gln Pro Arg Ser Val Pro 145	150
480	CCC TCC CCA GCT GAC ATC ACC CAT Pro Ser Pro Ala Asp Ile Thr His 160	165
528	GCC CAC GCT GCA CCC AGC ACC ACC Ala His Ala Ala Pro Ser Thr Thr 180	
576	GCT GCC GCT GCC GAC GCC GCA GCT Ala Ala Ala Ala Asp Ala Ala Ala 195	

Fig. 2(iii)

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GAC	AGG	GCT	GCC	ACT	CCC	CAC	CAC	431	
Asp	Arg	Ala	Ala	Thr	Pro	His	His		
140									
GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	479	
Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala		
155									
CCC	ACT	CCA	GCC	CCA	GGC	CCC	TCT	527	
Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser		
170								175	
AGC	GCC	CTG	ACC	CCC	GGA	CCT	GCC	575	
Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala		
185								190	
TCC	TCC	GTT	GCC	AAG	GGC	GGG	GCT	T	624
Ser	Ser	Val	Ala	Lys	Gly	Gly	Gly	Ala	
200								205	

Fig. 2(iv)

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625	AGAGCTCAAC CCAGACACCT GCAGGTGCCG
685	GACTCAGCAG GGTGACTTGC CTCAGAGGCT
745	GGTAAAAAAC AGCCAAGCCC CCAAGACCTC
805	GCCTCTCAGA GGGCTCTTCT GCCATCCCTT
865	GAGTTGGAAG AGGAGACTGG GAGGCAGCAA
825	GGAGTACTGT CTCAGTTCT AACCACTCTG
985	CTCCCCTCAC TAAGAAGACC CAAACCTCTG
1045	CTGTGACCCCC CAACCCTGAT AAAAGAGATG

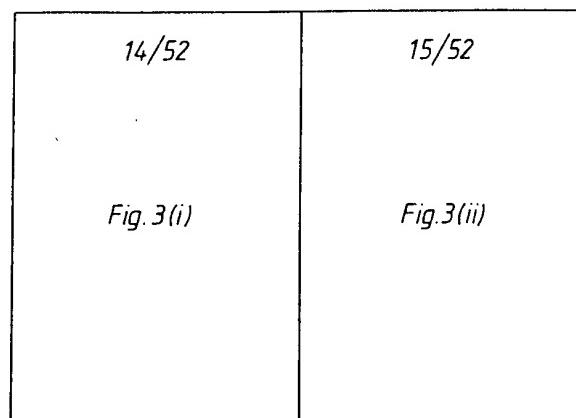
*Fig. 2(v)*

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GAAGCTGCGA AGGTGACACA TGGCTTTCA	684
ATATCCCAGT GGGGAAACAA AGGGGAGCCT	744
AGCCCAGGCA GAAGCTGCTC TAGGACCTGG	804
GTCTCCCTGA GGCCATCATC AAACAGGACA	864
GAGGGGTCAC ATACCAGCTC AGGGGAGAAT	924
TGCAAGTAAG CATCTTACAA CTGGCTCTTC	984
CATAATGGGA TTTGGGCTTT GGTACAAGAA	1044
GAAGGAAAAA AAAAAAAAAAA	1094

*Fig.2(vi)*

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>VEGF\_HUMAN VEGF\_HUMAN VASCULAR ENDOTHELIAL  
(VASCULAR 215 AA.  
LENGTH = 215

SCORE = 181 (92.4 BITS), EXPECT = 6.4e-20,  
IDENTITIES = 33/75 (44%), POSITIVES = 48/75

QUERY: 31 HQRKVVSVIDVYTRATCQPREVVPLTVEL  
+++ VV +DVY R+ C+P E +V + E  
SBJCT: 36 NHHEVVKFMDVYQRSYCHPIETLVDIFQEY

QUERY: 91 PTGQHQVRMQILMIR 105  
PT + + MQI+ I+  
SBJCT: 96 PTEESNITMQIMRIK 110

SCORE = 76 (38.8 BITS), EXPECT = 0.0011,  
IDENTITIES = 12/19 (63%), POSITIVES = 16/19

QUERY: 110 QLGEMSLEEHSQCECRPKK 128  
++GEMS +H+ CECRPKK  
SBJCT: 116 HIGEMSFLQHNKCECRPKK 134

SCORE = 72 (36.8 BITS), EXPECT = 0.0046,  
IDENTITIES = 14/21 (66%), POSITIVES = 15/21

QUERY: 202 RCQGRGLELNPDTCRCKLRR 222  
RC +R LELN TCRC K RR  
SBJCT: 195 RCKARQLELNERTCRCDKPRR 215

SCORE = 46 (23.5 BITS), EXPECT = 47.,  
IDENTITIES = 6/10 (60%), POSITIVES = 9/10

QUERY: 187 DPRTCRCKR 196  
DP+TC+C C+  
SBJCT: 181 DPQTCKCSCK 190  
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Fig.3(i)

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## GROWTH FACTOR PRECURSOR (VEGF)

P = 6.4e-20  
(64%)

MGTVAQLVPSCVTVQRCGGCCPDDGLECV 90  
+ PSCV + RCGGCC D+GLECV  
PDEIEYIFKPSCVPLMRCGGCCNDEGLECV 95

POISSON P(2) = 9.1e-12  
(84%)

POISSON P(3) = 3.6e-18  
(71%)

POISSON P(4) = 7.3e-10  
(90%)

Fig. 3(i)

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17/52	18/52
<i>Fig. 4(i)</i>	<i>Fig. 4(ii)</i>
19/52	20/52
<i>Fig. 4(iii)</i>	<i>Fig. 4(iv)</i>

18/52

TGCTCGCCGCACT.....CC	67
...TGGGTGCATTGGAGCCTTGCCT	56
TGTCTCCCAGCCTGATGCCCTGGC	117
GTGGTCCCAGGCTGCA.CCCATGGC	105
.AAGTGGTG....TCATGGATAGAT	147
GAAGTGGTGAAGTTCATG....GAT	151
CCCCGGGAG...GTGGTGGTGCCCT	193
CCAATCGAGACCCTGGTGGACATCT	200
GGGCACCGTGGCAAACAGCTGGTG	234
GTACATCTT...CAA.....G	238
GTGGTGGCTGCTGCCCTGACGATGG	284
GCGGGGGCTGCTGCAATGACGAGGG	288
CACCAAGTCCGGATGCAGAT.....	329
TCCAACATCACCATGCAGATTATGC	338

*Fig.4(ii)*  
SUBSTITUTE SHEET (RULE 26)

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Gap Weight:3.00      Average Match:1.000  
 Length Weight:0.100      Average Mismatch:-0.900  
 Quality:100.9      Length:739  
 Ratio:0.175      Gaps:30  
 Percent      Percent  
 Similarity:69.703      Identity:69.703

28	ATGAGCCCTCTGCTCCGCCGCCTGC 
17	ATGAACCTTCTGCT.....GTCT..
68	TGCAGCTGGCCCCCGCCCAGGCC 
57	TGCTGCTCTACCTCCACCATGCCAA
118	CACCAGAGGA..... 
106	AGAAGGAGGAGGGCAGAACATCAC
140	GTGTATACTCGC.GCTACCTGCCAG 
152	GTCTATCAGCGCAGCTA.CTGCCAT
194	T.....GA.....CTGTGGAGCTCAT 
201	TCCAGGAGTACCCCTGATGAGATCGA
235	CCCAGCTGCGTGACTGTGCAGCGCT 
239	CCATCCTGTGTGCCCTGATGCGAT
285	CCTGGAGTGTGTGCCCACTGGGCAG 
289	CCTGGAGTGTGTGCCCACTGAGGAG

Fig.4(i)

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330	.....CCTCATGATCCGGTACC 
339	GGATCAAACCTCA.....C
369	GTCCTGGAAAGAACACAGCCAGTGT 
376	GAGCTTCCTACAGCACAAACAATGT
419	GTGCTGTGAAGCCAGACAGGGCTGC 
423	G.....AGCAAGACAAG.....
469	CGTTCTGTTCCGGGCTGGGACTCTG 
443	...TGTGGGCCTTGCTCAGA.....
519	CATCACCCATCCCACCTCCAGCCCCA
468	.....
569	GC.....ACCACCAGCGCCC 
469	GCATTGTTGTACAA.....
609	TGCCGACGCCGCAGCTTCCTCCGTT 
509	TG.CAAAAAACACAGACTC..GCGTT
657	AACCCAGACACCTGCAGGTGCCGGA 
554	AACGAACGTACTTGCAGATGTGACA

Fig.4(iii)

20/52

CGAGCAGTCAGC . . . TGGGGGAGAT	368
CAAG . . GCCAGCACATAGGAGAGAT	375
GAATGCAGACCTAAAAAAAAGGACA	418
GAATGCAGACC . . . AAAGAAAGATA	422
CACTCCCCACCACCGTCCCCAGCCC	468
..... AAAATCCC . . . . .	442
CCCCCGGAGCACCCTCCCCAGCTGA	518
... GCGGAGAA . . . . .	467
GGCCCCCTCTGCCAACGCTGCACCCA	568
..... A	468
TGACCCCCGGACCTGCCGCTGCCGC	608
. GATCCCGAGACGTGTAAATGTTCC	508
GCCAAGGGCGGGGC . . TTAGAGCTC	656
GC . . AAGGCGAGGCAGCTTGAGTTA	553
AGCTGCGAAGGTGA	695
AGCCGAGGCGGTGA	592

Fig.4(iv)

**SUBSTITUTE SHEET (RULE 26)**

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22/52	23/52	24/52
<i>Fig.5(i)</i>	<i>Fig.5(ii)</i>	<i>Fig.5(iii)</i>
25/52	26/52	27/52
<i>Fig.5(iv)</i>	<i>Fig.5(v)</i>	<i>Fig.5(vi)</i>

22/52

165SOMSQ.MSF.msf MSF:687  
 Type: D Tuesday, June 20, 1995  
 Check:3140

	1
VEGF165	ATGAACCTTCTGCTGTCTGGGTG
SOM175	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6&7	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e4	ATGAGCCCTCTGCTCCGCCGCCTG
	81
VEGF165	CACCCATGGCAGAAGGAGGAGGGC
SOM175	TGCCCTGGCCACCAGAGGAAAGT
SOM175-e6	TGCCCTGGCCACCAGAGGAAAGT
SOM175-e6&7	TGCCCTGGCCACCAGAGGAAAGT
SOM175-e4	TGCCCTGGCCACCAGAGGAAAGT
	161
VEGF165	CCAATCGAGACCCTGGTGGACATC
SOM175	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6&7	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e4	GTGGTGGTGCCCTTGACTG.TGGA
	241
VEGF165	GATGCGATGCCGGGGCTGCTGCAA
SOM175	GCAGCGCTGTGGTGGCTGCTGCC
SOM175-e6	GCAGCGCTGTGGTGGCTGCTGCC
SOM175-e6&7	GCAGCGCTGTGGTGGCTGCTGCC
SOM175-e4	GCAGCGCTGTGGTGGCTGCTGCC

Fig.5(i)

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CATTGGAGCCTTGCCTGCTGCTCTACC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC

AGAATCATCACGAAGTGGTGAAGTTCAT  
GGTGTCATGGATAGATGTGTATACTCGC  
GGTGTCATGGATAGATGTGTATACTCGC  
GGTGTCATGGATAGATGTGTATACTCGC  
GGTGTCATGGATAGATGTGTATACTCGC

TTCCAGGAGTACCTGATGAGATCGAGT  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC

TGACGAGGGCCTGGAGTGTGTGCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCACT

*Fig. 5(ii)*

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80

TCCACCATGCCAAGTGGTCCCAGGCTG.  
CCGCCAGGCCCTGTCTCCCAGCCTGA  
CCGCCAGGCCCTGTCTCCCAGCCTGA  
CCGCCAGGCCCTGTCTCCCAGCCTGA

160

GGATGTCTATCAGCGCAGCTACTGCCAT  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG

240

ACATCTTCAAGCCATCCTGTGTGCCCT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT

320

GAGGAGTCCAACATCACCATGCAGATTA  
GGGCAGCACCAAGTCCGGATGCAGATCC  
GGGCAGCACCAAGTCCGGATGCAGATCC  
GGGCAGCACCAAGTCCGGATGCAGA...

Fig.5(iii)

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	321
VEGF165	TGC GGATCAAACCTCACCAAGGCC
SOM175	TCATGATCCGG...TACCCGAGCA
SOM175-e6	TCATGATCCGG...TACCCGAGCA
SOM175-e6&7	TCATGATCCGG...TACCCGAGCA
SOM175-e4	.....
	401
VEGF165	AAGAAAGATAG.....AGCAA
SOM175	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e6&7	AAAAAGGACAGTGCTGTGAAGCCA
SOM175-e4	AAAAAGGACAGTGCTGTGAAGCCA
	481
VEGF165	.....AAGCA.....
SOM175	CTCTGCCCGGGAGCACCCCTCCCC
SOM175-e6	.....
SOM175-e6&7	.....
SOM175-e4	CTCTGCCCGGGAGCACCCCTCCCC
	561
VEGF165	A.....GATCCGCA
SOM175	GCACCACCAGCGCCCTGACCCCCG
SOM175-E6	GCACCACCAGCGCCCTGACCCCCG
SOM175-e6&7	.....
SOM175-e4	GCACCACCAGCGCCCTGACCCCCG
	641
VEGF165	TTGAGTTAACGAACGTACTTGCA
SOM175	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6	TAGAGCTCAACCCAGACACCTGCA
SOM175-e6&7	.....
SOM175-e4	TAGAGCTCAACCCAGACACCTGCA

*Fig.5(iv)*

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AGCACATAGGAGAGATGAGCTTCCTACA  
GTCAGCTGGGGAGATGTCCCTGGAAGA  
GTCAGCTGGGGAGATGTCCCTGGAAGA  
GTCAGCTGGGGAGATGTCCCTGGAAGA  
.....

GACAAGAA.....AATCCCTGTGG.....  
GACAGGGCTGCCACTCCCCACCACCGTC  
GATAG.....  
GATAG.....  
GACAGGGCTGCCACTCCCCACCACCGTC

.....  
AGCTGACATCACCCATCCCACTCCAGCC  
.....CC  
.....  
AGCTGACATCACCCATCCCACTCCAGCC

GACGTGTAAATGTTCCCTGCACAAAC.AC  
GACCTGCCGCTGCCGCTGCCGACGCCGC  
GACCTGCCGCTGCCGCTGCCGACGCCGC  
.....

GACCTGCCGCTGCCGCTGCCGACGCCGC

687

GATGTGACAAGCCGAGGCAGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA  
.GTGCCGGAAGCTGCGAAGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA

*Fig.5(v)*

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400

GCACAACAAATGTGAATGCAGACC...A  
ACACAGCCAGTGTGAATGCAGACCTAAA  
ACACAGCCAGTGTGAATGCAGACCTAAA  
ACACAGCCAGTGTGAATGCAGACCTAAA  
.....CCTAAA

480

.....GCCTTGCTCAGAGCGGAGA  
CCCAGCCCCGTTCTGTTCCGGGCTGGGA  
.....  
.....  
CCCAGCCCCGTTCTGTTCCGGGCTGGGA

560

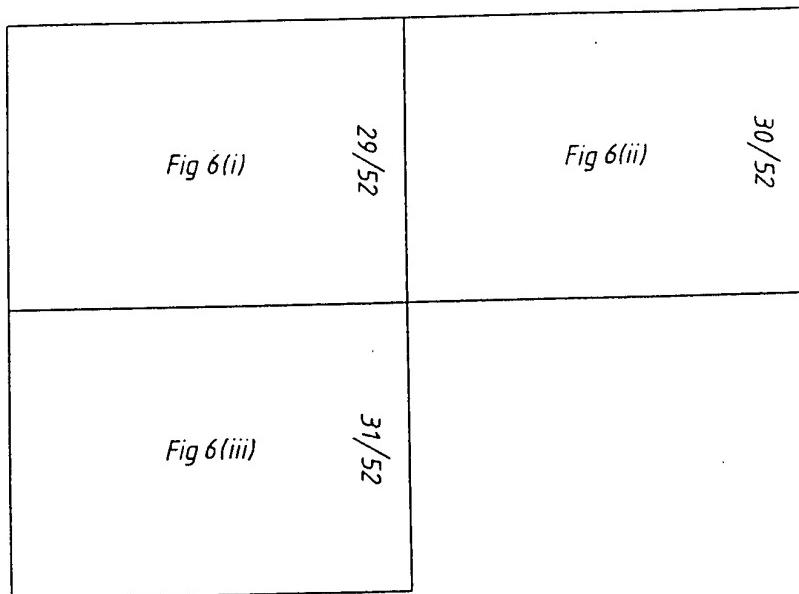
.....TTTGTT.....TGTAC..A  
CCAGGGCCCTCTGCCAACGCTGCACCCA  
CCAGGGCCCTCTGCCAACGCTGCACCCA  
.....  
CCAGGGCCCTCTGCCAACGCTGCACCCA

640

AGACTCG..CGTTGCAAGGCGAGGCAGC  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT  
.....  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT

*Fig.5(vi)*

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VEGF <sub>165</sub> SOM175 Short	M N F [L L S W V H W S [L A L L Y [L H H [A K W S Q A [A P M S P [L R R I L . . L A A L Q [L A P [A Q . . . A P
VEGF <sub>165</sub> SOM175 Short	I F Q [E Y P D E I E Y I F K P S C V P L M R C G G C C N L T V [E L M G T V A K Q L V P S C V T V Q R C G 3 C C P
VEGF <sub>165</sub> SOM175 Short	F L Q [H N K C E C R P K K . . . D R A . . . D R A A T P H H L E H S Q C E C R P K K K D S A V K P D R A A T P H H
VEGF <sub>165</sub> SOM175 Short	C K C S C K N T D S R C K A R Q L E L N E R T C R C D K H A A P S T T S A L T P G P A A A A D A A S S V A K
OR . . .	
VEGF <sub>165</sub> SOM175 Long	M N F [L L S W V H W S [L A L L Y [L H H [A K W S Q A [A P M S P [L R R I L . . L A A L Q [L A P [A Q . . . A P
VEGF <sub>165</sub> SOM175 Long	I F Q [E Y P D E I E Y I F K P S C V P L M R C G G C C N L T V [E L M G T V A K Q L V P S C V T V Q R C G G C C P
VEGF <sub>165</sub> SOM175 Long	F L Q [H N K C E C R P K K . . . D R A . . . D R A A T P H H L E E H S Q C E C R P K K K D S A V K P D R A A T P H H
VEGF <sub>165</sub> SOM175 Long	G P [C S E R R K H L F V Q D P Q [T C K C S C K N T D S . P R C T Q H H Q R . . . P D P R T C R C R C R R S F L

Fig. 6(i)

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PCT/AU96/00094

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M A E G G G Q N H	H E .	V V K F M D V Y Q R S Y C H P I E T L V D	60
V S Q P D A P G H	Q R K	V V S W I D V Y T R A T C C P R E V V V P	55
D E G L E C V P T	E E S N I	T M Q I M R I K P H Q G Q H I G E M S	121
D D G L E C V P T	G Q V R M Q	I L M I R . Y P S S Q L G E M S	115
· · · · ·	R Q E N P C G P C S E R R K H L F . V Q D P Q T	170	
R P Q P R S V P G W D S A P G A P S P A D I T H P T P A P G P S A	175		
P R R G G A			191 207

Fig. 6 (ii)

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Areas of 100% homology are boxed and conserved residues thought to be involved in homodimerisation are underlined. The VEGF sequence depicted includes the 26 amino acid leader sequence (removal of which gives rise to mature VEGF<sub>165</sub>) giving a total length of 191 amino acids.

Homology of SOM175 to VEGF<sub>165</sub> is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF). i.e.

Cysteine-47  
Proline-70, Cysteine-72, Valine-74  
Arginine-77, Cysteine-78, Glycine-80, Cysteines-81 & 82  
Cysteine-89, Proline-91  
Cysteines 122 & 124

Fig.6(iii)

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## SPLICING VARIANTS OF SOM175

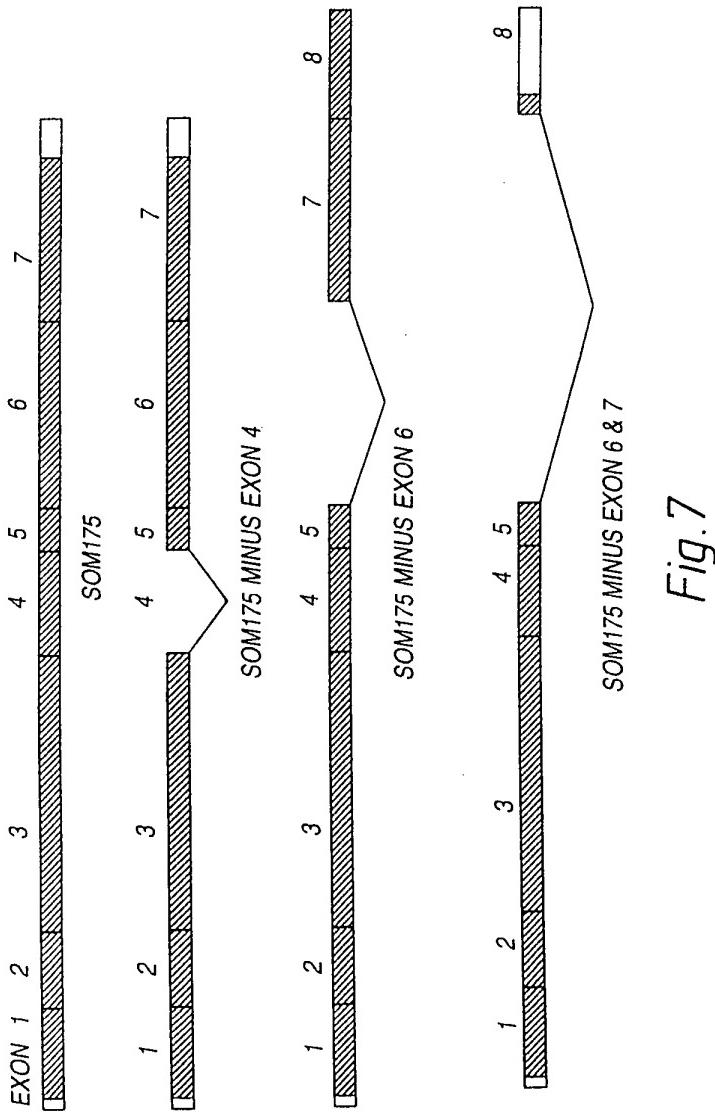


Fig. 7

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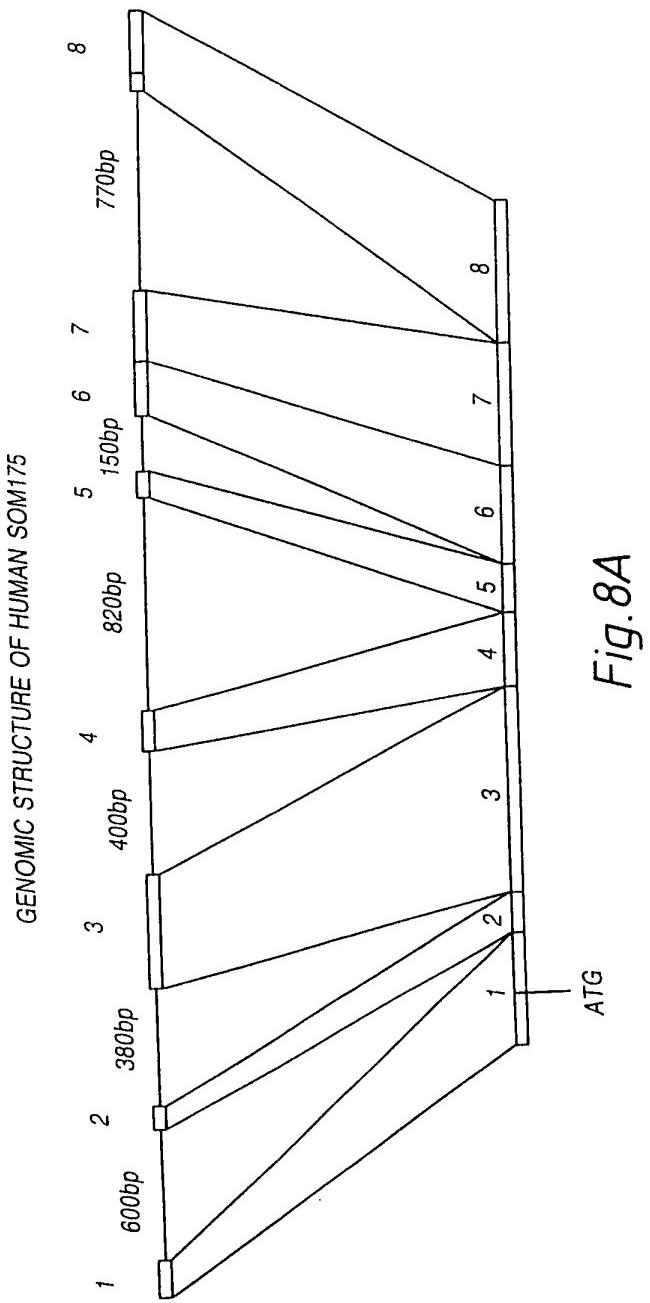


Fig. 8A

5' UTR . . . ATGAGG \*Exon 1 (60bp) GCCCAG gtacgttaggg

tctcccacag GCCCT Exon 2 (43bp) GGAAAG aataactaca  
tctgctccca TGGTGT Exon 3 (187bp) ATGCAG gtcccgaggatg  
ctgaatacag ATCCTC Exon 4 (73bp) ATGCAG gtgtcaggca  
actttcaag ACCTAA Exon 5 (34bp) AGACAG gtgagtttt  
ctcctccgta GGCTGC Exon 6 (101bp) CTCCAG ccccaggccc  
ccccactccag CCCCAG Exon 7 (109bp) ACCCAG acacacctgttag  
ccctgctcag GTGCCG \*Exon 8 (22bp) AGGTGA . . . 3' UTR

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PCT/AU96/00094

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36/52	37/52
<i>Fig. 9(i)</i>	<i>Fig. 9(ii)</i>
38/52	39/52
<i>Fig. 9(iii)</i>	<i>Fig. 9(iv)</i>

36/52

-163	gcacgagctcaggccgtcgctgcggcgctg
-103	ggggggccgcggaggagccgcggccctgcgcc
-43	ggcggctctggctgacccccccacacccg
16	CGTCGCCTGCTGCTTGCAC TGCTGCAG R R L L L V A L L Q
76	TTTGATGGCCCCAGTCACCAGAAGAAAGTG F D G P S H Q K K V
136	ACATGCCAGCCCAGGGAGGTGGTGGTGCCT T C Q P R E V V V P
196	AAACAAC TAGTGC CCAGCTGTGTGACTGTG K Q L V P S C V T V
256	GGCCTGGAATGTGTGCCACTGGGCAACAC G L E C V P T G Q H
316	TACCCGAGCAGTCAGCTGGGGAGATGTCC Y P S S Q L G E M S
376	CCTAAAAAAAAGGAGAGTGCTGTGAGGCCA P K K K E S A V R P
436	<u>CAGCCCCGCTCTGTTCCGGGCTGGGACTCT</u> Q P R S V P G W D S

Fig.9(i)

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cgttgcgctgcctgcggccaggcgtcgga  
 ccgccccgggtccccgggtccgcgcacatgg  
 ccgggctagggccccATGAGCCCCCTGCTG  
    M S P L L -17  
 ↓  
 CTGGCTCGCACCCAGGCCCCCTGTGTCCCAG  
 L A R T Q A P V S Q 4  
 GTGCCATGGATAGACGTTATGCACGTGCC  
 V P W I D V Y A R A 24  
 CTGAGCATGGAACTCATGGGCAATGTGGTC  
 L S M E L M G N V V 44  
 CAGCGCTGTGGTGGCTGCTGCCCTGACGAT  
 Q R C G G C C P D D 64  
 ↓  
 CAAGTCCGAATGCAGATCCTCATGATCCAG  
 Q V R M Q I L M I Q 84  
 ↓  
 CTGGGAGAACACAGCCAATGTGAATGCAGA  
 L G E H S Q C E C R 104  
 ↓  
 GACAGGGTGTGCCATAACCCACCACCGTCCC  
 D R V A I P H H R P 124  
ACCCCCGGGAGGCACCCCTCCCCAGCTGACATC  
 T P G A P S P A D I 144

Fig.9(ii)

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496	<u>ATCCATCCCAC</u> TCCAGCCCCAGGATCCTCT I H P T P A P G S S S P R I L
556	CTGACCCCCCGGACCTGCCGTTGCCGCTGTA L T P G P A V A A V P D P R T C R C R C
616	GGGG <u>CCTT</u> AGAGCTCAACCCAGACACCTGTA G A * R G L E L N P D T C
676	ctttccagactccacgggccccggctgtttt
736	agcacaggcgtaaacctcctcagtctggag
796	gagctctctcgccatcttttatctcccaga
856	atgtctcacctcagggccagggtactctc
916	ttctggctggctgtctcccctcaactatgaa
976	gggttctgttatgataactgtg <u>acacacac</u>
1036	gacactaaaaaaaaaaaaaaaaaaaaaaa

Fig.9(iii)

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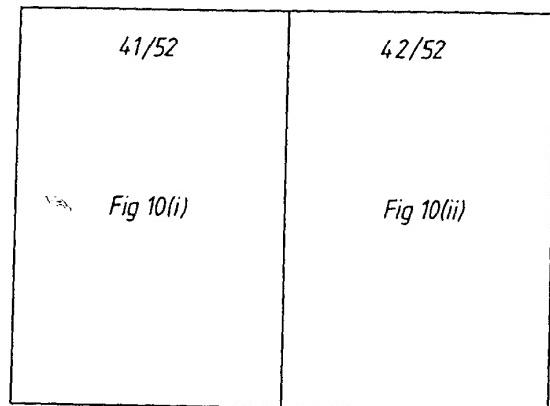
GCCCGCCTTGCACCCAGCGCCGCCAACGCC	
A R L A P S A A N A	164
C P P C T Q R R Q R	130
GACGCCGCGCTTCCTCCATTGCCAAGGGC	
D A A A S S I A K G	184
R R R R F L H C Q G	150
↓	
GGTGCCCGGAAGCCGCGAAAG <u>TG</u> Acaagctg	186
R C R K P R K *	167
tatggccctgcttcacaggagaagagtgg	
gtcactgccccaggacacctggacctttaga	
gctgccatctaacaattgtcaaggaacctc	
tcacttaaccaccctggtcaagtgagcatc	
aaccccaaacttctaccaataacgggattt	
acacactcacact <u>gtaaaa</u> agagatgga	
aaaaaaaaaaaaaa	

Fig.9(iv)

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A

hVRF167	-21	MSPLLRRLLLALLQLAPAQAP 
mVRF167	-21	MSPLLRRLLLVALLQLARTQAP
hVRF167	30	EVVVPLTVELMGTVAKQLVPSC       :
mVRF167	30	EVVVPLSMELMGNVVKQLVPSC
hVRF167	80	ILMIRYPSSQLGEMSLEEHSQC                   :
mVRF167	80	ILMIQYPSSQLGEMSLGEHSQC
hVRF167	130	RPDPRTCRCRCKRRSFLRCQGR                       :
mVRF167	130	RPDPRTCRCRCKRRRFLHCQGR

B

Fig. 10(i)

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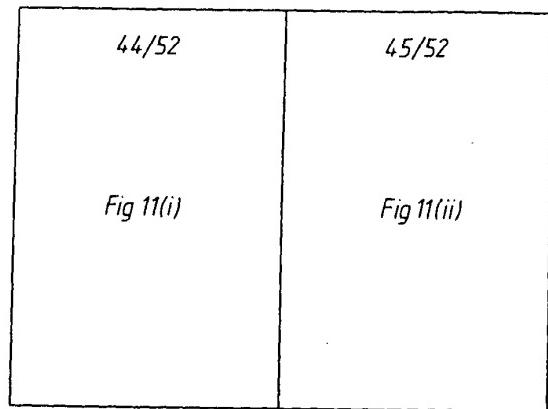
VSQPDAPGHQRKVWSWIDVYTRATCQPR	29
:     :	
VSQFDGPGSHQKKVVPWIDVYARATCQPR	29
:     :	
VTVQRCGGCCPDDGLECVPTGQHQVRMQ	79
:     :	
VTVQRCGGCCPDDGLECVPTGQHQVRMQ	79
ECRPKKDSAVKPDSPRPLCPRCTQHHQ	129
:     :                :	
ECRPKKKESAVRPDSPRILCPPCTQRRQ	129
GLELNPDTCRCKLRR*	167
:     :	
GLELNPDTCRCKPRK*	167
APSPADITHPTPAPGPSAHAAPSTTSAL	165
:	
APSPADIIPHPTPAPGSSARLAPSAAANAL	165
186	
186	

Fig. 10(ii)

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mVRF167	-21	MSPLLRRLL..LLVALLQL..
		::   :
mVEGF188	-26	MNFLLSWVHWTLALLYLHH
mVRF167	25	TCQPREVVVPLSMELMGNVV
		:  :   :::
mVEGF188	24	YCRPIETLVDIFQEYPDEIE
mVRF167	75	QVRMQILMIQYPSSQ.LGEM
		:    :       :
mVEGF188	74	NITMQIMRIKPHQSQHIGEM
mVRF167	119	.....ILCPPC
		:
mVEGF188	124	QKRKRKKSRFKSWSVHCEPC
mVRF167	152	GLENPDTCRCKPRK
		:
mVEGF188	173	QLELNERTCRCDKPRR

Fig.11(i)

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AR.TQAPVSQFDGPSHQKKVVPWIDVYARA	24
:  : :  : :  :	
AKWSQAAPTT.EGEQKSHEVIKFMDVYQRS	23
KQLVPSCVTVQRCGGCCPDDGLECVPTGQH	74
:     :   :     ::     ::	
YIFKPSCVPLMRCAGCCNDEALECVPTSES	73
SLGEHSQCECRPKKESAVRPDSPR.....	118
: :	
SFLQHSRCECRPKKDRTKPEKKSVRGKGKG	123
TQRRQR...PDPRTCRCRRCRRRFHLHCQGR	151
:   :      :   : :  :	
SERRKHLFVQDPQTCKCSCKNTDS.RCKAR	172
	167
	188

Fig.11(ii)

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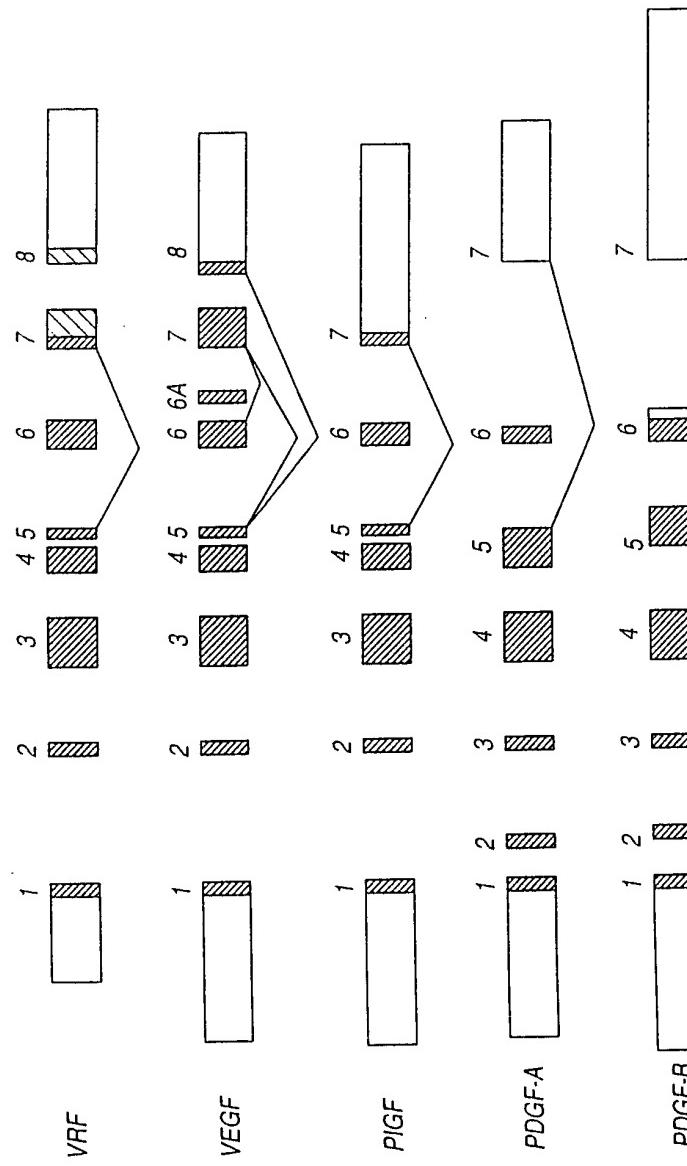


Fig. 12

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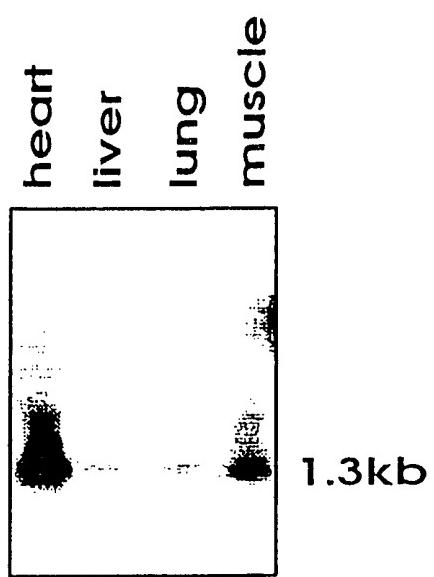


Fig. 13

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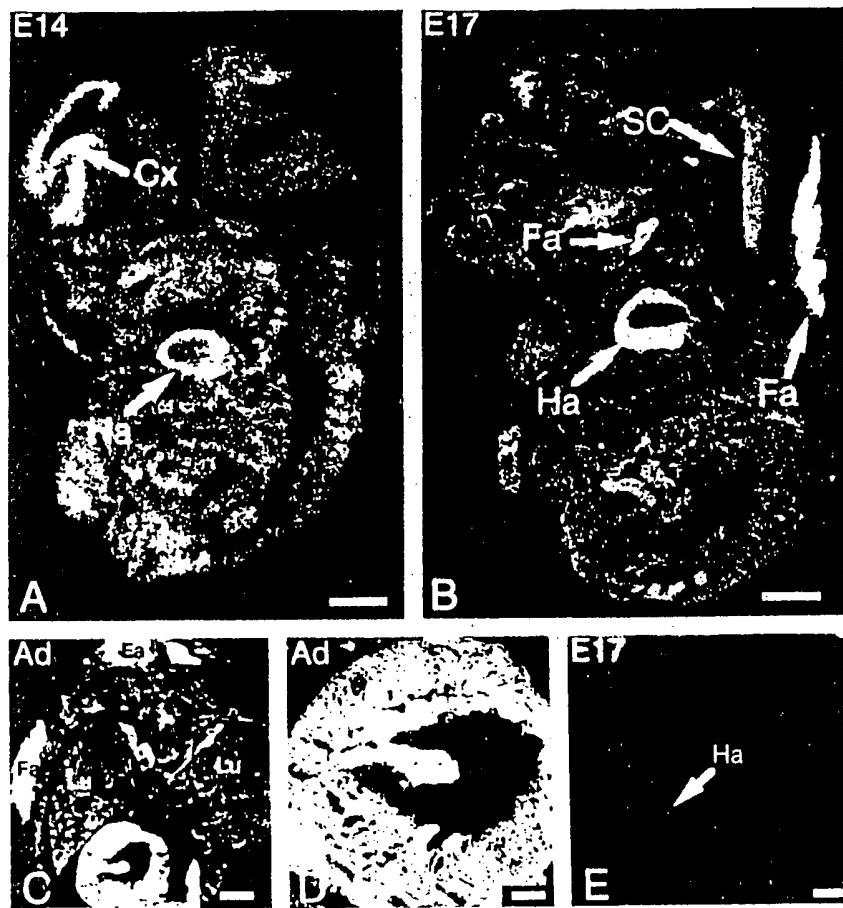


Fig.14

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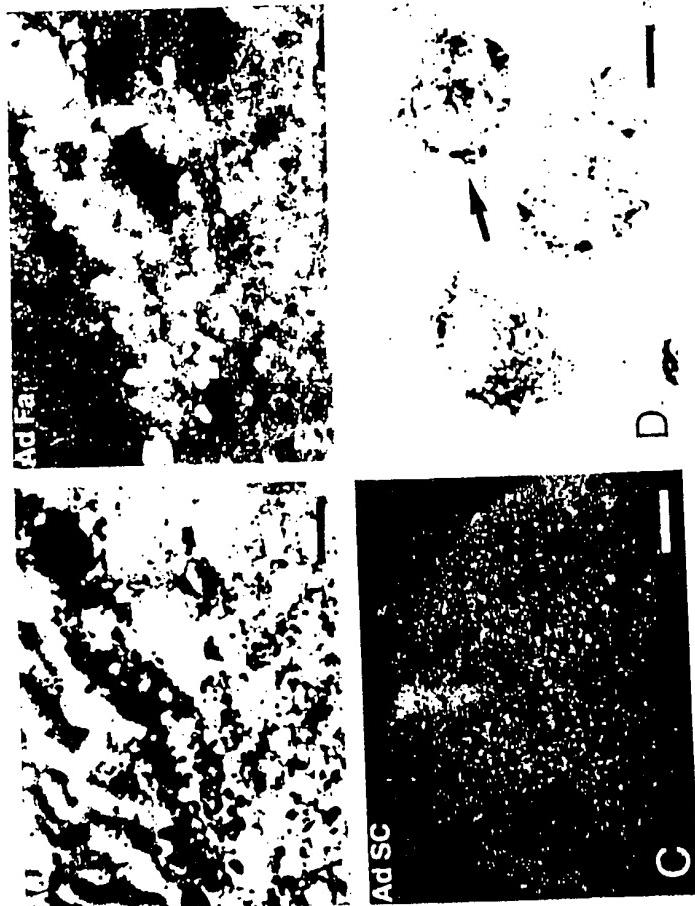


Fig. 15

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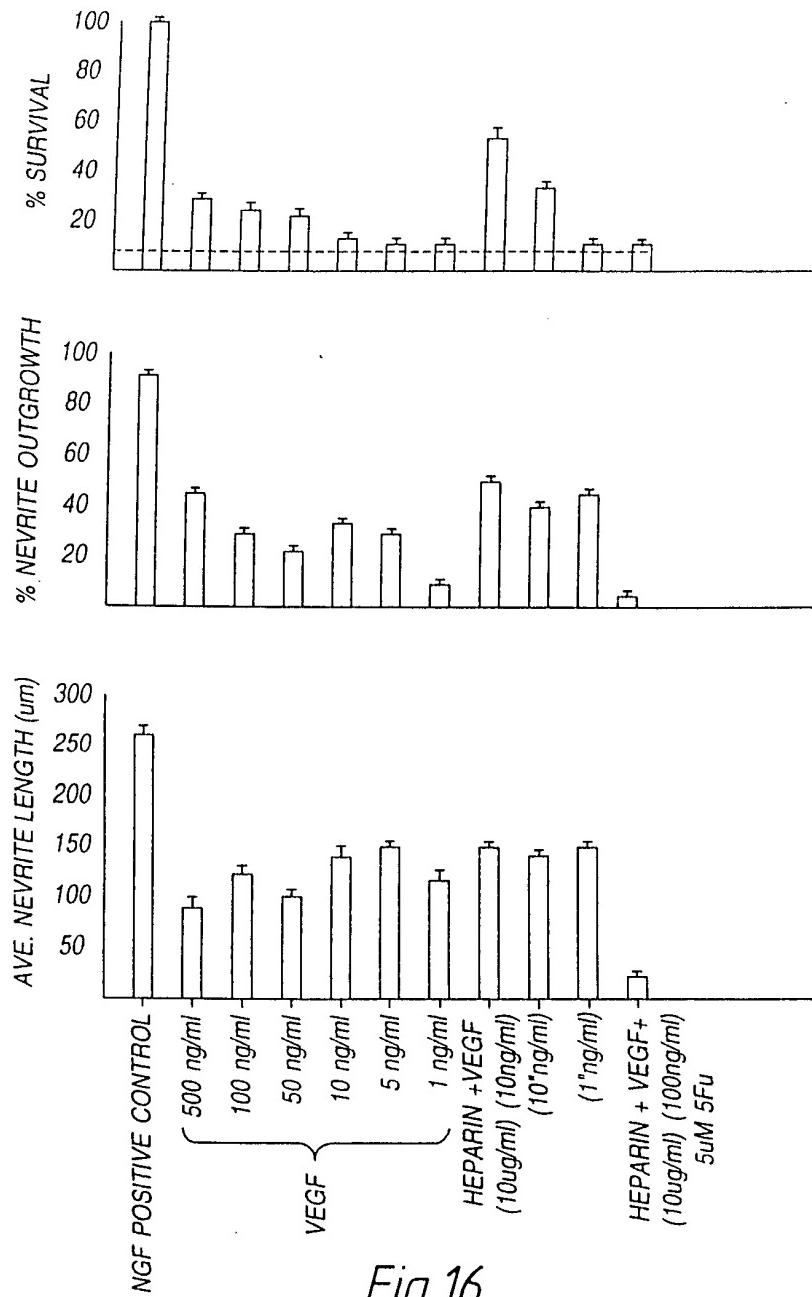


Fig. 16

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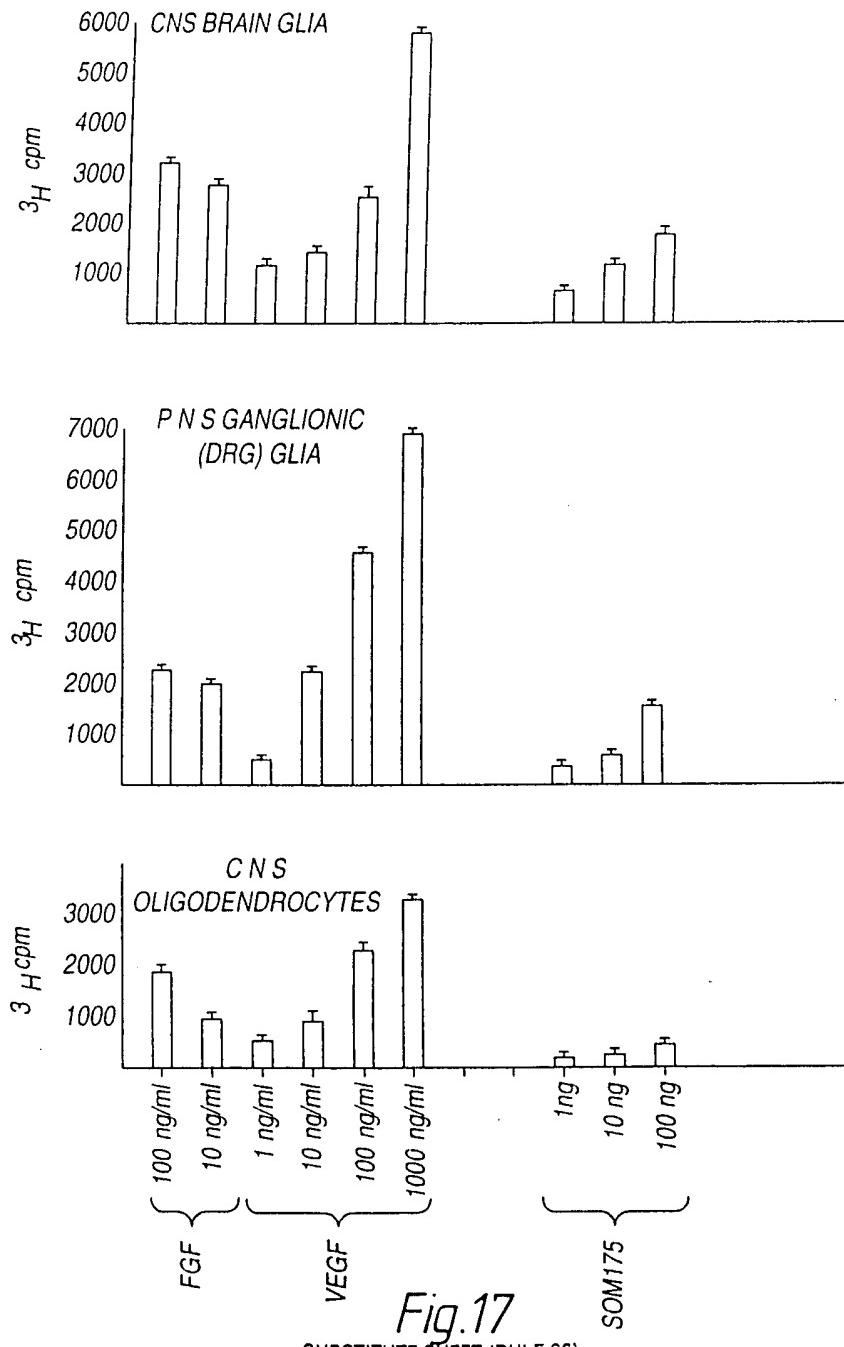


Fig. 17

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## MOUSE ASTROGLIAL CELLS

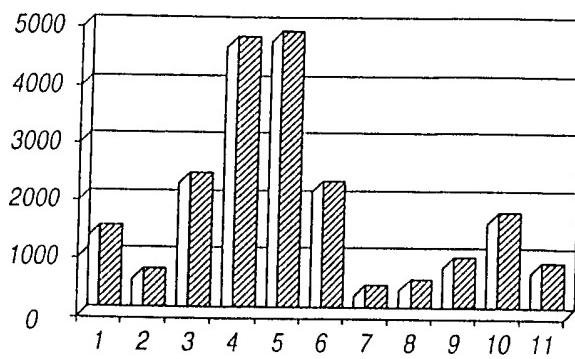


Fig.18

## MOUSE OLIGODENDROGLIAL CELLS

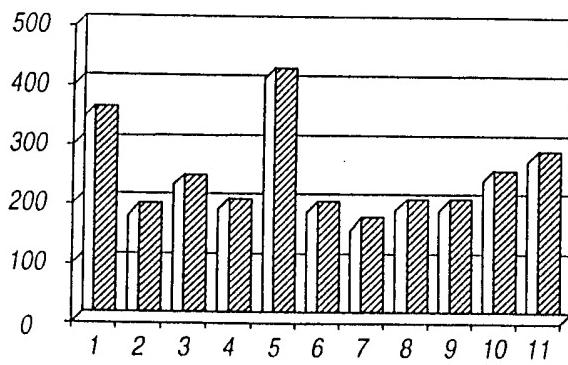


Fig.19

## MOUSE FOREBRAIN NEURONS

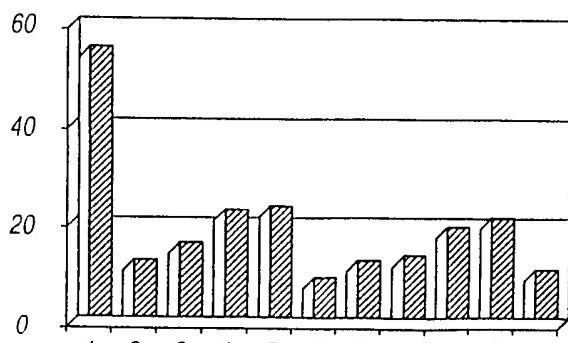


Fig.20